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Supplemental Methods:

SARS-CoV-2 viral antigen multiplexed binding assay

To measure antibody levels to SARS-CoV-2 spike subunit proteins (spike subunit 1 (S1), spike subunit 2 (S2), receptor-binding domain (RBD)) antigens, we utilized a bead-based multiplex assay based on the Luminex xMAP technology using reagent kits that had secondary antibodies that were specific for immunoglobulin isotypes (IgG). We used the following kit: IgG (Millipore, #HC19SERG1-85K) following standard manufacture protocols. Each kit provided the same sets of SARS-CoV-2 antigen conjugated beads (S1, S2, RBD) along with 4 positive control beads and a negative control bead set. The positive control beads were beads coated with different concentrations of IgG. The negative control beads did not have antigen conjugated to determine nonspecific binding. The 4 antigen-conjugated beads, 4 positive control beads and 1 negative control beads were mixed and incubated with each plasma sample that were diluted 1:100 with assay buffer. With each assay plate, at least two sample wells with only buffer and no plasma were included to determine assay background. Finally, PE-anti-human IgG conjugate detection antibodies were utilized to determine antibody isotype responses to each of the SARS-CoV-2 antigens. Using the positive control beads we determined the inter-assay (plate-to-plate) coefficient of variation (CV) for each assay. We determined that the CVs were 5.16% for the assays, respectively. In order to acquire and analyze data we utilized the Luminex analyzer (MAGPIX) and Luminex xPONENT acquisition software. Samples were run in technical duplicate and after acquisition Net MFI was utilized which is MFI with background well (no plasma) MFI subtracted. Positive control beads were utilized to ensure positive detection of the well and to identify any inter- and/or intra-assay technical variation. We next determined the level of nonspecific binding by using the negative control samples MFI (beads without antigen mixed with plasma).

SARS-CoV-2 viral neutralizing antibody assays

To detect viral neutralizing antibodies the SARS-CoV-2 Surrogate Virus Neutralization Test kit was utilized (Genscript, #L00847) according to the standard protocol. Samples were run in duplicate with blocking values averaged. This kit detects antibodies that can block the interaction between the receptor binding domain of the viral spike glycoprotein with the Angiotensin Converting Enzyme 2 (ACE2) cell surface receptor and has been

approved by the FDA for emergency use. Plasma samples along with positive (anti-RBD antibody) and negative (buffer only) were incubated with a Horseradish peroxidase (HRP) conjugated recombinant SARS-CoV-2 RBD fragment. The mixture was then added to a capture plate that was coated with the human ACE2 protein. The unbound HRP-RBD will bind to the plate. After washing, 3,3',5,5'-Tetramethylbenzidine (TMB) solution was added to develop the HRP signal and was read at 450 nm in a microtiter plate reader. The absorbance of the sample is inversely dependent on the titer of the anti-SARS-CoV-2 neutralizing antibodies. Inhibition was calculated by (1- OD value of sample/ OD value of negative control) x 100 which gives percent inhibition. A cutoff of ≥30% is considered positive for SARS-CoV-2 neutralizing antibody. Plasma samples were diluted 1:10 for all samples.

Statistical analysis

Descriptive statistics and group differences were determined at each timepoint using a nonparametric ungrouped Wilcoxon-Mann-Whitney test that was corrected for multiple comparisons (FDR). Graphpad prism (v9) was used to generate graphs and perform statistical tests.

In order to calculate decay rates and antibody half-life and exponential model was used. "lmer" function available in the lme4 (v1.1-27.1) package was used for designing the model. The statistical model used in R for Fixed Effect:

For COVID-19 titer

Model = lme4::lmer(log10(Titer) ~ Weeks + (1|StudyID) -1, data = AntibodyTiterData)

For RBD, SI and S2

Model = lme4::lmer(log10(Titer) ~ Weeks + (1|StudyID) , data = AntibodyTiterData)

Intercept value, also known as decay rate, for weeks was obtained after running the above model.

To obtain Half-life:

log10(0.5)/Intercept (decay rate) was used.

Reported confidence interval and Akaike Information Criterion (AIC) were obtained with R base function "confint" and "AIC" respectively.

Table S1. Study participant demographics

	Recent SARS-CoV-2 infection (N=36)	**No history of infection** (N=152)
Age	Median 38 years old Range 25-73 years old	Median 46 years old Range 22-75 years old
Gender	Male: 4 Female: 32	Male: 46 Female: 105
Race	White: 34 Black or African American: 0 American Indian or Alaska Native: 0 Asian: 2 Native Hawaiian or Other Pacific Islander: 0 Multiracial: 0 Unknown: 0	White: 133 Black or African American: 3 American Indian or Alaska Native: 0 Asian: 7 Native Hawaiian or Other Pacific Islander: 0 Multiracial: 5 Unknown: 4
Ethnicity	Hispanic or Latino: 5 Not Hispanic or Latino: 30 Unknown: 1	Hispanic or Latino: 10 Not Hispanic or Latino: 129 Unknown: 13

Table S2. 95% Confidence interval of median of binding antibody responses

No infection	Week 7	Week28
S1	Lower: 26,185 Upper: 27,270	Lower: 7,373 Upper: 9,643
S2	Lower: 22,711 Upper: 23,858	Lower: 10,951 Upper: 13,737
RBD	Lower: 25,871 Upper: 26,525	Lower:14,437 Upper: 17,138

Recent infection	Week 7	Week28
S1	Lower: 27,154 Upper: 29,147	Lower: 10,246 Upper: 18,043
S2	Lower: 29,513 Upper: 32,502	Lower: 18,350 Upper: 24,684
RBD	Lower: 25,295 Upper: 26,885	Lower: 18,581 Upper: 24,000

Table S3. 95% Confidence interval of median of RBD blocking antibody responses

Week	No infection	Recent infection
Week 7	Lower: 95.91 Upper: 96.74	Lower: 97.73 Upper: 97.89
Week 16	Lower: 89.91 Upper: 93.00	Lower: 96.37 Upper: 97.25
Week 24	Lower: 82.51 Upper: 88.97	Lower:93.77 Upper: 97.55
Week 28	Lower: 63.52 Upper: 72.30	Lower:77.89 Upper: 87.84

Table S4. Exponential decay model values for binding antibodies

S1 protein

Estimate	Std. Error	t value	2.50%	97.50%	AkaikeInformationCriterion	Group
-0.0126686	0.00132395	-9.5688225	-0.0152873	-0.0100442	-68.787452	Recent infection
-0.0221373	0.00085652	-25.845682	-0.0238215	-0.0204542	-197.86712	No infection

S2 protein

Estimate	Std. Error	t value	2.50%	97.50%	AkaikeInformationCriterion	Group
-0.0068698	0.00070367	-9.7627521	-0.0082669	-0.0054783	-128.48663	Recent infection
-0.0130485	0.00069214	-18.852433	-0.0144101	-0.011689	-280.52516	No infection

RBD

Estimate	Std. Error	t value	2.50%	97.50%	AkaikeInformationCriterion	Group
-0.0031034	0.0008794	-3.5290597	-0.0048432	-0.0013635	-132.27542	Recent infection
-0.0105675	0.00058869	-17.95101	-0.011725	-0.0094107	-381.76277	No infection

Table S5. Exponential decay model values for RBD blocking

Estimate	Std. Error	t value	2.50%	97.50%	AkaikeInformationCriterion	Group
-0.0022456	0.00022848	-9.8283994	-0.0027176	-0.0017935	-225.28226	Recent infection
-0.0063529	0.00038703	-16.414534	-0.0071478	-0.0055753	-373.14049	No infection

Estimate	Std. Error	t value	2.50%	97.50%	AkaikeInformationCriterion	Group
-0.0050277	0.00040084	-12.542896	-0.0058505	-0.0042273	-256.79704	18-49 years old
-0.0077994	0.00065845	-11.845183	-0.0091804	-0.006468	-132.86889	50+ years old